

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2023.023P** |  |
| **Short title:** Establish a new species in the genus *Nanovirus* (family *Nanoviridae*) |
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**Author(s) and email address(es)**

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**List the ICTV Study Group(s) that have seen this proposal**

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| *Nanoviridae* SG |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
| Nanoviridae | 10/12 | 0/12 | 2/12 |
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**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | 19th June 2023 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2023.023P.A.v1\_Nanovirus\_1nsp.xlsx |

**Abstract**

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| Milk vetch chlorotic dwarf virus was identified in Iran from two symptomatic milk vetch (*Astragalus myriacanthus* Boiss.) samples (sample ID G50 and G53; sampled in 2018) showing marginal leaf chlorosis, reduced leaf size and dwarfing symptoms. These two nanoviruses represent a new species in the family *Nanoviridae*. |

**Text of proposal**

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| A new nanovirus, milk vetch chlorotic dwarf virus (MVCDV), was identified in Iran from two symptomatic milk vetch (*Astragalus myriacanthus* Boiss.) samples (sample ID G50 and G5). These were sampled in 2018 from Nafech in Chaharmahal and Bakhtiari province of central Iran, and showed marginal leaf chlorosis, small leaves and dwarfing symptoms [1]. Each genome component of the G50 and G53 share 84.4 - 99.7% pairwise identity, determined using SDT v1.2 [2] with the counterpart component sequences. The genomes (concatenated component sequences) of MVCDV share 62.2-74.7% pairwise identity with all other nanoviruses (Figure 1). The CPs encoded by DNA-S of MVCDV share 78.6-85.0% amino acid sequence identity with those of black medic leaf roll virus (BMLRV) and 44-62% with those of all others nanovirus CPs.The species demarcation threshold for nanoviruses proposed by the ICTV Nanoviridae Study group [3-4] is >15% divergence in the CP amino acid sequence and/or nucleotide pairwise identity of overall genomes <75% when compared to other nanoviruses. The genome of MVCDV and that of BMLRV is close to 75% and the CP amino acid identity is <85%, both of which are close to the new species demarcation limits. The phylogenetic analysis (Figure 2) of the individual components coupled with the pairwise identity analysis supports the establishment of a new species to accommodate MVCDV.To conform with the binominal species names [5], we propose the name ***Nanovirus astragalirani*** (epithet is a contraction of host genus name *Astragalus* and Iran). The exemplar virus in this new species is milk vetch chlorotic dwarf virus isolate G53 with the following accession numbers: DNA-U4: MN273339DNA-U2: MN273338DNA-U1: MN273337DNA-R: MN273336DNA-N: MN273335DNA-M: MN273334DNA-S: MN273333DNA-C: MN273332  |

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**Supporting evidence**

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Black medic leaf roll virus – BMLRV

Cow vetch latent virus – CvLV

Faba bean necrotic stunt virus – FBNSV

Faba bean necrotic yellows virus – FBNY

Faba bean yellow leaf virus – FBYLV

Milk vetch chlorotic dwarf virus – MVCDV

Milk vetch dwarf virus – MVDV

Pea necrotic yellow dwarf virus, – PNYDV

Parsley severe stunt associated virus – PSSaV

Pea yellow stunt virus – PYSV

Subterranean clover stunt virus – SCSV

Sophora yellow stunt virus – SYSV

**Figure 1:** Pairwise identity matrix of the genome (concatenated component sequences) of representative nanoviruses determine using SDT v1.2 [2]. Figure adapted from Hassan-Sheikhi et al., [1].

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**Figure 2:** Maximum likelihood phylogenetic trees, inferred using PhyML [6] of MVCDV component nucleotide sequences and rooted with babuvirus sequences except for those of DNA-U1, DNA-U2 and DNA-U4 which are midpoint rooted. Figure adapted from Hassan-Sheikhi et al. [1].

**References**

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